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Using X-rays as a driven force to study chemical reduction on protein crystals

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Abstract content

Radiation damage to cryocooled protein crystals during x-ray structure determination has become an inherent part of macromolecular diffraction data collection at third-generation synchrotrons. Although it is possible to make use of this damage, for example for radiation damage-induced phasing (RIP), in the majority of cases radiation damage is an unwelcome part of data collection. X-rays interact with matter in three ways. The X-ray photons may be absorbed via the photoelectric effect, scattered inelastically (Compton scattering) or scattered elastically (Thomson scattering). Only the last of these contributes to the useful part of the observed diffraction pattern. The dominant interaction at energies typically used in macromolecular crystallography is the photoelectric effect, which accounts for more than 80% of the total interaction, with around 8% being due to Compton scattering. Therefore most of the X-rays interacting with the crystal deposit their energy into it, causing radiation damage. As a consequence of those interactions, almost every protein crystal is chemically reduced, emphasizing its effect in the vicinities of metallic atoms. For this reason the crystallographic studies focused on metallo enzymes has to be performed in a very precise and careful way, taking advantage of the apparent limitations and exploited them in order to describe the system. Such approaches would be explained, as well as the importance of synchrotron radiation in order to perform them.

Summary

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